

# Implementation of the inference algorithm

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 An abbreviated version of this protocol was published in eLIFE in Nov 2014

Predicting evolution from the shape of genealogical trees

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## Detailed protocol

Thank you for your interest in our paper. With more recent versions of fasttree, modification of the code should no longer be necessary. Instead, you can compile it with a flag indicating double precision:

<http://www.microbesonline.org/fasttree/#BranchLen>

Regarding the outgroup, you could use a strain from the early 1990ies like this one:

[https://www.fludb.org/brc/fluStrainDetails.spg?strainName=A/Beijing/32/1992\(H3N2\)&decorator=influenza](https://www.fludb.org/brc/fluStrainDetails.spg?strainName=A/Beijing/32/1992(H3N2)&decorator=influenza)

**How to cite:** (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Neher, R. and Shraiman, B. (2020). Implementation of the inference algorithm. Bio-protocol Preprint. [bio-protocol.org/prep350](https://bio-protocol.org/prep350).
2. Neher, R. A., Russell, C. A. and Shraiman, B. I.(2014). Predicting evolution from the shape of genealogical trees. eLIFE. DOI: [10.7554/eLife.03568](https://doi.org/10.7554/eLife.03568)

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